AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-4. (cancelled).

5. (currently amended): A method for detecting a SARS coronavirus in a sample, comprising: (1) ~~amplifying~~ amplification of a target nucleic acid region of the SARS coronavirus consisting of the nucleotide sequence of SEQ ID NO:1 using a first~~an~~ oligonucleotide primer comprising ~~at least 15 contiguous nucleotides of~~ SEQ ID NO:17~~,~~ or a nucleotide sequence entirely complementary ~~thereto~~to said first oligonucleotide primer, a second oligonucleotide primer comprising ~~at least 15 contiguous nucleotides of~~ SEQ ID NO:18~~,~~ or a nucleotide sequence entirely ~~complimentary thereto~~complementary to said second oligonucleotide primer, a third oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:10~~,~~ or a nucleotide sequence entirely ~~complimentarythereto~~complementary to said third oligonucleotide primer, and a fourth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:19~~,~~ or a nucleotide sequence entirely ~~complimentary thereto~~complementary to said fourth oligonucleotide primer; (2) detecting a product of said target nucleic acid amplification, and wherein the detection of said product indicates that said sample contains a SARS coronavirus.

6. (canceled).

7. (currently amended): ~~A~~ The method of Claim 5, wherein said sample is obtained from an animal and wherein detection of a SARS coronavirus in said sample indicates that said animal is afflicted with ~~for diagnosing~~ severe acute respiratory syndrome (SARS) ~~comprising diagnosing infection with the SARS coronavirus by detecting amplification of a target nucleic acid region of the SARS coronavirus using the oligonucleotide primers according to claim 5~~.

8 - 11. (canceled).

12. (currently amended): The method of claim 5, wherein said first, second, third and fourth primers comprise a nucleotide sequence of SEQ ID NO:1 selected from the following nucleotide sequences (a) to (d), provided that ~~the~~ an F3c, ~~the~~ an F2c, and ~~the~~ an F1c ~~regions~~ region ~~are~~ is selected from the 3'-terminus and ~~the~~ an R3, ~~the~~ an R2, and ~~the~~ an R1 ~~regions~~ region ~~are~~ is selected from the 5'-terminus of the target nucleic acid of the SARS coronavirus, and nucleotide sequences entirely complementary ~~thereto~~ to each of said primers are determined to be F3, F2, and F1 and R3c, R2c, and R1c, respectively:

(a) a nucleotide sequence having ~~the~~ an F2 region and ~~the~~ an F1c region of the target nucleic acid at the 3'-terminus and the 5'-terminus, respectively;

(b) a nucleotide sequence having ~~the~~ an F3 region of the target nucleic acid;

(c) a nucleotide sequence having ~~the~~ an R2 region and ~~the~~ an R1c region of the target nucleic acid at the 3'-terminus and the 5'-terminus, respectively; and

(d) a nucleotide sequence having ~~the~~ an R3 region of the target nucleic acid.

13 - 20. (cancelled).

21. (currently amended): The method according to claim 5, further comprising a fifth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:22, or a nucleotide sequence entirely ~~complimentary thereto~~complementary to said fifth oligonucleotide primer, and a sixth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:23, or a nucleotide sequence entirely complementary ~~complimentary thereto~~to said sixth oligonucleotide primer.